

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2004, 17:25:48 ; Search time 335 Seconds

(without alignments)

6684.445 Million cell updates/sec

Perfect score: 459

Sequence: 1 gtcatgcctgtatggctcat.....gtcccttcaggattctctag 459

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 3191023 seqs, 2439312756 residues

Total number of hits satisfying chosen parameters:

6382046

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications\_NA.\*

1: /cgn2\_6/ptodata/2/pubprna/2/pubprna/PCT\_NEW\_PUB.seq:\*

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3: /cgn2\_6/ptodata/2/pubprna/2/pubprna/US06\_NEWPUBCOMB.seq:\*

4: /cgn2\_6/ptodata/2/pubprna/2/pubprna/US06\_NEWPUBCOMB.seq:\*

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12: /cgn2\_6/ptodata/2/pubprna/2/pubprna/US09\_NEWPUB.seq:\*

13: /cgn2\_6/ptodata/2/pubprna/2/pubprna/US09\_NEWPUB.seq:\*

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18: /cgn2\_6/ptodata/2/pubprna/2/pubprna/US60\_NEWPUB.seq:\*

19: /cgn2\_6/ptodata/2/pubprna/2/pubprna/US60\_NEWPUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	459	100.0	459	9	US-09-975-607A-2
2	459	100.0	459	13	US-09-974-919C-2
3	436	95.0	486	9	US-09-975-607A-1
4	436	95.0	486	13	US-10-389-821-9
5	348	75.8	3163	13	US-10-116-802-291
6	348	75.8	3163	15	US-10-084-817-252
7	348	75.8	3198	13	US-10-058-270A-79
8	348	75.8	3198	15	US-10-177-293-58
9	348	75.8	3226	9	US-09-954-456-725
10	348	75.8	3226	13	US-10-240-425-1543
11	348	75.8	3285	16	US-10-295-027-109
12	340.4	74.2	636	15	US-10-198-846-8437
13	340.4	74.2	3368	15	US-10-198-846-10814
14	336	73.2			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT	1	US-09-975-607A-2	ALIGNMENTS
		Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
		Searched: 3191023 seqs, 2439312756 residues	
		Total number of hits satisfying chosen parameters:	
		6382046	
		Minimum DB seq length: 0	
		Maximum DB seq length: 2000000000	
		Post-processing: Minimum Match 0%	
		Maximum Match 100%	
		Listing first 45 summaries	
		Published Applications_NA.*	
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RESULT 7  
 US-10-084-817-252  
 ; Sequence 252, Application US/10084817  
 ; Publication No. US2003011900911  
 ; GENERAL INFORMATION  
 ; APPLICANT: Susan Stuart  
 ; APPLICANT: Jed G. Nuchtern  
 ; APPLICANT: Sharon E. Plon  
 ; APPLICANT: Jason M. Shohet  
 ; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION  
 ; FILE REFERENCE: PA-0046 US  
 ; CURRENT APPLICATION NUMBER: US/10/084-817  
 ; CURRENT FILING DATE: 2002-02-25  
 ; PRIOR APPLICATION NUMBER: 60/270,784  
 ; PRIOR FILING DATE: 2001-02-23  
 ; NUMBER OF SEQ ID NOS: 365  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO: 252  
 ; LENGTH: 3163  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US2003011900911 982520.1  
 ; NAME/KEY: unsure  
 ; LOCATION: 806  
 ; OTHER INFORMATION: a, t, c, g, or other  
 ; US-10-084-817-252

Query Match 75.8%; Score 348; DB 13; Length 3198;  
 Best Local Similarity 85.6%; Pred. No. 3e-113;  
 Matches 404; Conservative 0; Mismatches 55; Indels 13; Gaps 1;

Qy 1 GTCATGCTGATGGCTCATAGGCGCAGGGCCAGGCTTGTGGATGCCCTT 60  
 Db 1659 GTCATGCTGAGGGTTTATAAGGGAGCCAAAGGCCAGCTTCTGGACCCCTT 1718  
 Qy 61 GTCAAGGTAAACACGGGTAACAGGTAACTGGTGTCTGCTTACTGTCATTCTCT 120  
 Db 1719 GTTAGGGCCAACGGGGTAACAGGAATGCTGCTGTTACTGTTACTGTTCTCC 1778  
 Qy 121 AAAGCTTACCCAGGCTTACGGTGTGCTTACCCATTGATGAGATTCTGTCATAATAGGCAG 180  
 Db 1779 AAAGCTTACCCAGGAATAGGAATACCTTACATTGATAAAATTTGATAACGGCA 1838  
 Qy 181 CAGCATTACGCCAAGATCAGGTATCTTACCTGTAAGATGCCAGGATATACATTTC 240  
 Db 1839 CAGCATTATGACCCAAAGACTGAAATCTTACTGTCATAACGGCA 1896  
 Qy 241 TCCTTACCACTGTCATGTGAAAGGACTCACGTTGGCTAGGCTGTATAAGAACGGC--- 297  
 Db 1798 TCATACCACGTCATGTGAAAGGACATGTTGGCTAGGCTGTATAAGAACGGCA 1857

RESULT 8  
 US-10-058-270A-79  
 ; Sequence 79, Application US/10058270A  
 ; Publication No. US2004002911A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Afar, Daniel  
 ; APPLICANT: BioTechnology, Inc.  
 ; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and Methods of Screening for Modulators of Breast Cancer  
 ; FILE REFERENCE: 018501-005210US  
 ; CURRENT APPLICATION NUMBER: US/10/058,270A  
 ; PRIOR APPLICATION NUMBER: US 60/263,965  
 ; PRIOR FILING DATE: 2001-01-24  
 ; PRIORITY NUMBER: US 60/265,928  
 ; PRIORITY NUMBER: US 60/288,472  
 ; PRIORITY NUMBER: US 60/282,698  
 ; PRIORITY NUMBER: US 60/288,590  
 ; PRIORITY NUMBER: US 60/294,443  
 ; NUMBER OF SEQ ID NOS: 141  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 79  
 ; LENGTH: 3198  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-058-270A-79

Query Match 75.8%; Score 348; DB 13; Length 3198;  
 Best Local Similarity 85.6%; Pred. No. 3e-113;  
 Matches 404; Conservative 0; Mismatches 55; Indels 13; Gaps 1;

Qy 1 GTCATGCTGATGGCTCATAGGCGCAGGGCTTCTGGATGCCCTT 60  
 Db 1558 GTCATGCTGAGGGTTTATAAGGGAGCCAAAGGCCAGCTTCTGGACCCCTT 1617  
 Qy 61 GTCAGGTCTAACCGGGTAACTGGTGTCTGCTTACTGTCATTCTCT 120  
 Db 1618 GTTAGGTCACCCAGGGTAAAGGAATGCTGTCTGCTTACTGTTATCTCC 1677  
 Qy 121 AAAGCTTACCCAGGATAGGGTGTGCCCATCCATTGATGAGATTCTGTCATAATAGGCAG 180  
 Db 1678 AAAGCTTACCCAGGATAGGGTGTGCCCATCCATTGATGAGATTCTGTCATAATAGGCAG 1737  
 Qy 181 CAGCATTACGCCAAGATCTGTCATTCTCTGTCATAACGGCA 240  
 Db 1738 CAGCATTATGCCAAGACTGAAATTTACTGTCATAACGGAAATACTATTTC 1797  
 Qy 241 TCCTTACCACTGTCATGTGAAAGGACTCACGTTGGCTAGGCTGTATAAGAACGGC--- 297  
 Db 1798 TCATACCACGTCATGTGAAAGGACATGTTGGCTAGGCTGTATAAGAACGGCA 1857

Qy 298 -----ACACGTATGAGTACAGCAAAAGGCTACCTGEGATCAAGCTCAGGGAGT 347  
 Db 1858 CCTGTAATGTRACCTATGATAAACCAAGGCTACCTGGATCAGGAGT 1917  
 Qy 348 GCAATCATGGAGTCAGAAATGACCAAGGTATGGCTCAATTGCAATGAGATCA 407  
 Db 1918 GCAATCATGATCTCAGAAATGACCAAGGTGTGCTCCAAATGCCAGTCA 1977  
 Qy 408 AAGGCCCTRACTCTGAGTCACTGCTGCTCTCAGGATTCCTAG 459  
 Db 1978 AATGGCCTATRACTCTGAGTCACTCCTCTCAGGATTCCTAG 2029

RESULT 9  
 US-10-177-293-58  
 ; Sequence 58, Application US/10177293  
 ; PUBLICATION NO. US20030124128A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lillie, James  
 ; APPLICANT: Glatt, Karen  
 ; APPLICANT: Zhao, Xumei  
 ; APPLICANT: Gannavarpu, Manjula  
 ; APPLICANT: Matkar, Shubhangi  
 ; APPLICANT: Mertens, Maureen  
 ; APPLICANT: Myer, Vic  
 ; APPLICANT: Wang, Youzhen  
 ; APPLICANT: Xu, Yongyao  
 ; APPLICANT: Hoersch, Sebastian  
 ; APPLICANT: Nonahan, John  
 ; APPLICANT: Meyers, Rachel E.  
 ; APPLICANT: Bast Jr., Robert C.  
 ; APPLICANT: Horobogay, Gabrielle N.  
 ; APPLICANT: Puszta, Lajos  
 ; APPLICANT: Meric, Funda  
 ; APPLICANT: Sabin, Ayesegul  
 ; APPLICANT: Mills, Gordon B.  
 ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER  
 ; FILE REFERENCE: MRI-038  
 ; CURRENT APPLICATION NUMBER: US/10/177,293  
 ; CURRENT FILING DATE: 2002-06-21  
 ; PRIORITY APPLICATION NUMBER: US 60/299,887  
 ; PRIORITY FILING DATE: 2001-06-21  
 ; PRIORITY APPLICATION NUMBER: US 60/301,572  
 ; PRIORITY FILING DATE: 2001-06-27  
 ; PRIORITY APPLICATION NUMBER: US 60/306,501  
 ; PRIORITY FILING DATE: 2001-07-18  
 ; PRIORITY APPLICATION NUMBER: US 60/325,002  
 ; PRIORITY FILING DATE: 2001-09-25  
 ; PRIORITY APPLICATION NUMBER: US 60/362,585  
 ; PRIORITY FILING DATE: 2002-03-05  
 ; PRIORITY APPLICATION NUMBER: US 60/xxxx,xxx  
 ; PRIORITY FILING DATE: 2002-05-14  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO: 58  
 ; LENGTH: 3198  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-177-293-58

Qy 121 AAAGCTTACCCAGCAGTAGGTGCCCATCCATTGATGAGATTCTGTACATAGGGAG 180  
 Db 1678 AAAGCTTACCCAGCAATAGGAATCCTCCATACATTGATATAACGGCA 1737  
 Qy 181 CAGCATTAAGGCAAGATCTGTATTTACCTGTAGATCCAGGATATACTATTC 240  
 Db 1738 CAGCATATGCCAAGGACTGAATCCAGGATATACTATTCAGATACCTATT 1797  
 Qy 241 TCTTACACGTGATGTGAAAGGACTCACTGTTGGCTGTATAAGACGCC--- 297  
 Db 1798 TCTACACGTGATGTCAAAGGACTATGTGGTAGGCTGTATAAGATGGAC 1857  
 Qy 298 -----ACACGTATGAGTACAGCAAAAGGCTACCTGEGATCAAGCTCAGGGAGT 347  
 Db 1858 CCTGTAATGTRACCTATGATAAACCAAGGCTACCTGGATCAGGAGT 1917  
 Qy 348 GCAATCATGGAGTCAGAAATGACCAAGGTATGGCTCAATTGCAATGAGATCA 407  
 Db 1918 GCAATCATGATCTCAGAAATGACCAAGGTGTGCTCCAAATGCCAGTCA 1977  
 Qy 408 AAGGCCCTRACTCTGAGTCACTGCTGCTCTCAGGATTCCTAG 459  
 Db 1978 AATGGCCTATRACTCTGAGTCACTCCTCTCAGGATTCCTAG 2029

RESULT 10  
 US-09-954-456-725  
 ; Sequence 725, Application US/09954456  
 ; PUBLICATION NO. US2010115057A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Paul  
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer Cells  
 ; CURRENT APPLICATION NUMBER: US/09/954,456  
 ; PRIORITY APPLICATION NUMBER: US/60/233,617  
 ; PRIORITY FILING DATE: 2001-09-18  
 ; PRIORITY APPLICATION NUMBER: US/60/233,617  
 ; PRIORITY FILING DATE: 2000-09-18  
 ; PRIORITY APPLICATION NUMBER: US/60/234,052  
 ; PRIORITY FILING DATE: 2000-09-20  
 ; PRIORITY APPLICATION NUMBER: US/60/234,923  
 ; PRIORITY FILING DATE: 2000-09-25  
 ; PRIORITY APPLICATION NUMBER: US/60/235,134  
 ; PRIORITY FILING DATE: 2000-09-25  
 ; PRIORITY APPLICATION NUMBER: US/60/235,637  
 ; PRIORITY FILING DATE: 2000-09-26  
 ; PRIORITY APPLICATION NUMBER: US/60/235,638  
 ; PRIORITY FILING DATE: 2000-09-26  
 ; PRIORITY APPLICATION NUMBER: US/60/235,711  
 ; PRIORITY FILING DATE: 2000-09-27  
 ; PRIORITY APPLICATION NUMBER: US/60/235,720  
 ; PRIORITY FILING DATE: 2000-09-27  
 ; PRIORITY APPLICATION NUMBER: US/60/235,840  
 ; PRIORITY FILING DATE: 2000-09-27  
 ; PRIORITY APPLICATION NUMBER: US/60/235,863  
 ; PRIORITY FILING DATE: 2000-09-27  
 ; NUMBER OF SEQ ID NOS: 2276  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 725  
 ; LENGTH: 3226  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-954-456-725

Query Match 75.8%; Score 348; DB 15; Length 3198;  
 Best Local Similarity 85.6%; Pred. No. 3e-113; Gaps 1;  
 Matches 404; Conservative 0; Mismatches 55;

Qy 1 GTCATGCCCTGATGCCCTCATAAAGCAGGCCAGGGCCAGGTCTCTGGATGCCGCTT 60  
 Db 1558 GTCATGCCCTGAGGTTTAAAGCAGGCCAGGGCCAGGTCTCTGGATGCCGCTT 1617

Query Match 75.8%; Score 348; DB 9; Length 3226;  
 Best Local Similarity 85.6%; Pred. No. 3e-111; Gaps 1;  
 Matches 404; Conservative 0; Mismatches 55; Indels 13; Gaps 1;

Qy 1 GTCATGCCCTGATGCCCTCATAAAGCAGGCCAGGGCCAGGTCTCTGGATGCCGCTT 60  
 Db 1573 GTCATGCCCTGAGGTTTAAAGCAGGCCAGGGCCAGGTCTCTGGATGCCGCTT 1632

61	GTCAGTGTCAACCA CGGGTAACAGGTATGCCGTGTTACTGTATTCTCT	120	Db	1693	AAAGCTTACCGGAAATAGGAACCTCCATACCCATTGATCTTACCTGATAAAATTGTGATAACAGSCAA	1752	
1633	GTTAGTGCACCA CGGGGTAAACGAATGGCTGTTACTGTATTCTCT	1692	Qy	181	CAGCATAGGACCCAGATCTGGTATCTTACCTGTAAGTCAGTCCAGCATACTTTTC	240	
121	AAGCTTACCCAGCTAGGTGCCCATCCATTGATGAGATTCTGTAAATAGGCAG	180	Db	1753	CAGCATAGGACCCAGATCTGGTATCTTACCTGTAAGTCAGTCCAGCATACTTTTC	1812	
1693	AAGCTTACCCAGCTAGGTGCCCATCCATTGATGAGATTCTGTAAATAGGCAG	1752	Qy	181	CAGCATAGGACCCAGATCTGGTATCTTACCTGTAAGTCAGTCCAGCATACTTTTC	1752	
181	CAGCATACGGCCAGATGGTATCTTACCTGTAAGATCCAGCATACTATTTC	240	Db	241	TCCCTACAGGTGATGTGAAGGGACTCACTGTTACTGTGATGGCTTACGGCC	297	
1753	CAGCATACGGCCAGATGGTATCTTACCTGTAAGATCCAGCATACTATTTC	1812	Qy	241	TCCCTACAGGTGATGTGAAGGGACTCACTGTTACTGTGATGGCTTACGGCC	1872	
241	TCCCTACAGGTGATGTGAAGGGACTCACTGTTACTGTGATGGCTTACGGCC	297	Db	1813	TCTACACAGGTGATGTGAAGGGACTCACTGTTACTGTGATGGCTTACGGCC	1992	
1813	TCTACACAGGTGATGTGAAGGGACTCACTGTTACTGTGATGGCTTACGGCC	1872	Qy	298	-----ACAGTATGATGAGTACAGCAAAAGGTACTCTGGTCAATGCCAATGAGGAT	347	
298	-----ACAGTATGATGAGTACAGCAAAAGGTACTCTGGTCAATGCCAATGAGGAT	347	Db	1873	CCCTTAATSTACACCTATGATGATACCAAAAGGTACTCTGGTCAATGCCAATGAGGAT	1932	
1873	CCCTTAATSTACACCTATGATGATACCAAAAGGTACTCTGGTCAATGCCAATGAGGAT	1932	Qy	348	GCAATCTGGTCAATGCCAATGAGGATCTGGTCACTCTCAGGATTCCTAG	459	
348	GCAATCTGGTCAATGCCAATGAGGATCTGGTCACTCTCAGGATTCCTAG	407	Db	1933	GCATCATGATCTCACAGAAATGCAAGGTGCTCAGCTCCATGCCAATGAGGAT	2044	
1933	GCATCATGATCTCACAGAAATGCAAGGTGCTCAGCTCCATGCCAATGAGGAT	1992	Qy	408	AACGGCCTCTACTCTCTCAGTACGGTCAACTCTCAGGATTCCTAG	459	
Db	1993	AATGGCTTATACCTCTCAGTATGTCACACTCTCAGGATTCCTAG	2044	Db	1993	AATGGCTTATACCTCTCAGTATGTCACACTCTCAGGATTCCTAG	2044
RESULT 12							
US-10-295-027-109							
; Sequence 1.09, Application US/10295027							
; GENERAL INFORMATION:							
; APPLICANT: Afar, Daniel							
; APPLICANT: Aziz, Natasha							
; APPLICANT: Gansberg, Wendy M.							
; APPLICANT: Gish, Kurt C.							
; APPLICANT: Glynn, Richard							
; APPLICANT: Hevezsi, Peter A.							
; APPLICANT: Mack, David H.							
; APPLICANT: Murray, Richard							
; APPLICANT: Watson, Susan R.							
; APPLICANT: Eos Biotechnology, Inc.							
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and							
; GENERAL INFORMATION:							
; FILE REFERENCE: 018501-012500US							
; CURRENT FILING DATE: 2002-11-13							
; PRIORITY NUMBER: US 09/663,733							
; PRIORITY NUMBER: US 09/663,733							
; PRIORITY NUMBER: US 60/350,666							
; PRIORITY NUMBER: US 60/335,394							
; PRIORITY NUMBER: US 60/332,464							
; PRIORITY NUMBER: US 60/334,393							
; PRIORITY NUMBER: US 60/340,376							
; PRIORITY NUMBER: US 60/355,250							
; PRIORITY NUMBER: US 60/347,211							
; PRIORITY NUMBER: US 60/347,008							
; PRIORITY NUMBER: US 60/347,349							
; PRIORITY NUMBER: US 60/355,250							
; PRIORITY NUMBER: US 60/356,714							
; Remaining Prior Application data removed - See File Wrapper or PALM.							
; NUMBER OF SEQ ID NOS: 1386							
; SOFTWARE: PatentIn Ver. 2.1							
; SEQ ID NO: 109							
; LENGTH: 3285							
; TYPE: DNA							
; ORGANISM: Homo sapiens							
; US-10-295-027-109							
; Query Match							
; Best Local Similarity 75.8%; Score 348; DB 13; Length 3226;							
; Matches 404; Conservative 85.6%; Fred. No. 3e-113; Mismatches 0; Gaps 1;							
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 X60382							
; US-10-240-425-1543							
; FEATURE: TYPE: DNA							
; ORGANISM: Homo sapiens							
; FEATURE: FEATURE:							
; Query Match							
; Best Local Similarity 75.8%; Score 348; DB 13; Length 3226;							
; Matches 404; Conservative 85.6%; Fred. No. 3e-113; Mismatches 0; Gaps 1;							
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 X60382							
; US-10-240-425-1543							
; FEATURE: TYPE: DNA							
; ORGANISM: Homo sapiens							
; US-10-295-027-109							
; Query Match							
; Best Local Similarity 75.8%; Score 348; DB 13; Length 3226;							
; Matches 404; Conservative 85.6%; Fred. No. 3e-113; Mismatches 0; Gaps 1;							
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 X60382							
; US-10-240-425-1543							
; FEATURE: TYPE: DNA							
; ORGANISM: Homo sapiens							
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; Query Match							
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; ORGANISM: Homo sapiens							
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; Matches 404; Conservative 85.6%; Fred. No. 3e-113; Mismatches 0; Gaps 1;							
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; US-10-240-425-1543							
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; ORGANISM: Homo sapiens							
; US-10-295-027-109							
; Query Match							
; Best Local Similarity 75.8%; Score 348; DB 13; Length 3226;							
; Matches 404; Conservative 85.6%; Fred. No. 3e-113; Mismatches 0; Gaps 1;							
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 X60382							
; US-10-240-425-1543							
; FEATURE: TYPE: DNA							
; ORGANISM: Homo sapiens							
; US-10-295-027-109							
; Query Match							
; Best Local Similarity 75.8%; Score 348; DB 13; Length 3226;							
; Matches 404; Conservative 85.6%; Fred. No. 3e-113; Mismatches 0; Gaps 1;							
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 X60382							
; US-10-240-425-1543							
; FEATURE: TYPE: DNA							
; ORGANISM: Homo sapiens							
; US-10-295-027-109							
; Query Match							
; Best Local Similarity 75.8%; Score 348; DB 13; Length 3226;							
; Matches 404; Conservative 85.6%; Fred. No. 3e-113; Mismatches 0; Gaps 1;							
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 X60382							
; US-10-240-425-1543							
; FEATURE: TYPE: DNA							
; ORGANISM: Homo sapiens							
; US-10-295-027-109							
; Query Match							
; Best Local Similarity 75.8%; Score 348; DB 13; Length 3226;							
; Matches 404; Conservative 85.6%; Fred. No. 3e-113; Mismatches 0; Gaps 1;							
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 X60382							
; US-10-240-425-1543							
; FEATURE: TYPE: DNA							
; ORGANISM: Homo sapiens							
; US-10-295-027-109							
; Query Match							
; Best Local Similarity 75.8%; Score 348; DB 13; Length 3226;							
; Matches 404; Conservative 85.6%; Fred. No. 3e-113; Mismatches 0; Gaps 1;							
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 X60382							
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; ORGANISM: Homo sapiens							
; US-10-295-027-109							
; Query Match							
; Best Local Similarity 75.8%; Score 348; DB 13; Length 3226;							
; Matches 404; Conservative 85.6%; Fred. No. 3e-113; Mismatches 0; Gaps 1;							
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 X60382							
; US-10-240-425-1543							
; FEATURE: TYPE: DNA							
; ORGANISM: Homo sapiens							
; US-10-295-027-109							
; Query Match							



181 CAGCATTAGGCCAAGATACTGGTATCTTACCTGTAAGATCCAGGATAATACTATTTC 240  
 Qy 1910 CAGCATTAGGCCAAGACTGGTATCTTACCTGTAAGATCCAGGATAATACTATTTC 240  
 Db 1910 CAGCATTAGGCCAAGACTGGTATCTTACCTGTAAGATCCAGGATAATACTATTTC 459  
 Qy 241 TCCTTACCAAGCTCATGTGAAGGACTACAGTTGGTAGGCTGTATAAGAACGGC- 297  
 Db 1970 TCATACCAAGCTCATGTGAAGGACTACAGTTGGTAGGCTGTATAAGATGCCAC 2029  
 Qy 298 -----AGACGTATGATGAGTAAAGAACGGCTACCTGATAGGGTCAAGGGAGT 347  
 Db 2030 CCTGTAATGTCACCTATGATGATAACCCAAAGGCTACCTGGATAGGGAGT 2089  
 Qy 348 GCAATCATGGAGCTCAGAAATGACCAAGCTGATGGCTCCAAATTGCCAATGCCAGATA 407  
 Db 2090 GCAATCATGAACTCAAGAAATGACCAAGCTGATGGCTCCAGCTCCAGGCCAGTCA 2149  
 Qy 408 AACGGCTCTACTCCCTGASTACAGTCACGTCCCTCTAGGATCTCTAG 459  
 Db 2150 AATGGCCCTATACTCTGTGAGTGTCCACTCTCTAGGATCTCTAGGATCTCTAG 2201

RESULT 15

US-10-085-783A-38423  
 ; Sequence 38423, Application US/10085783A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chondrogen Inc.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/7305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271,955  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 38423  
 ; LENGTH: 465  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-085-783A-38423

Query Match 61.2%; Score 281; DB 13; Length 465;  
 Best Local Similarity 85.1%; Pred. No. 1.1e-89; Mismatches 1;  
 Matches 331; Conservative 0; Gaps 1;

Qy 84 AGGATGGCCGTTCTGTTTACTGTCTTCTCTCTAAAGCTTACCAAGCTAGTGTGC 143  
 Db 1 AGGAATGGCTGTCCTGTTTACTGTCTTCTCTCTAAAGCTTACCAAGCTAGTGTGC 60  
 Qy 144 CCCCATCCATTGTGAGATCTGTGAAATAGCGAGCAATTACGCCAAGATCTGG 203  
 Db 61 TCCATACATTGATAAATTTGTATAACGGCAAGCATTATGCCAAGGACTGG 120  
 Qy 204 TACCTTACCTGTAAGATCCAGGATAATCTCTTCTACCGCTGTGAAAGG 263  
 Db 121 AACCTTACCTGTAACCGGAAATATCTTCTACCTTCTACCGCTGTGAAAGG 180  
 Qy 264 GACTCACGTTGGTAGGCTGTATAAGATGCCCTGTAAATGTCACCTATGAGA 310  
 Db 181 GACTCATGTTGGTAGGCTGTATAAGATGCCCTGTAAATGTCACCTATGAGA 240  
 Qy 311 GTACAGCAAAAGGTACCTGGTACGGCTCAGGCTCAATCATGGCTCACAGAAA 370  
 Db 241 ATACCCAAAGGTACCTGGTAGGCTCAGGCTCACAGAAA 300  
 Qy 371 TGACCGGTATGGCTCCAAATTGCCAATCGAGATAACGGCTCTACTCCCTGAGTA 430

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.  
 OM nucleic - nucleic search, using sw model  
 Run on: July 20, 2004, 11:56:30 ; Search time 66 Seconds  
 (without alignments)  
 3859.431 Million cell updates/sec

Title: US-09-975-607a-2  
 Perfect score: 459  
 Sequence: 1 gtcattctgtatggcttcat.....gtcccttctcaaggatccatg 459

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:  
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 2: /cgna2\_6/ptodata/2/ina/5B COMB.seq.\*  
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 6: /cgna2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	436	100.0	459	4 US-09-415-551-2	Sequence 2, Appli
2	436	95.0	486	4 US-09-415-551-1	Sequence 1, Appli
3	133	29.0	2487	4 US-09-620-312D-160	Sequence 160, App
4	90.8	19.8	855	4 US-09-552-04A-10	Sequence 10, Appli
5	69	15.0	1313	2 US-08-463-911-6	Sequence 6, Appli
6	69	15.0	4517	3 US-09-140-804-9	Sequence 9, Appli
7	69	15.0	4517	4 US-09-686-38B-9	Sequence 5, Appli
8	69	15.0	4517	4 US-09-776-976-5	Sequence 5, Appli
9	69	15.0	4517	4 US-09-909-547-5	Sequence 5, Appli
10	69	15.0	4545	4 US-09-569-852B-5	Sequence 5, Appli
11	69	15.0	20966	4 US-09-776-976-7	Sequence 7, Appli
12	69	15.0	20966	4 US-09-909-547-7	Sequence 7, Appli
13	66.8	14.6	729	3 US-09-140-804-10	Sequence 1, Appli
14	66.8	14.6	729	4 US-09-686-38B-10	Sequence 10, Appli
15	66.8	14.6	729	4 US-09-776-976-3	Sequence 10, Appli
16	66.6	14.5	1152	4 US-09-776-976-1	Sequence 1, Appli
17	66.6	14.5	1152	4 US-09-909-547-1	Sequence 1, Appli
18	66.6	14.5	1276	2 US-08-463-911-1	Sequence 1, Appli
19	66.6	14.5	1276	4 US-09-776-976-3	Sequence 3, Appli
20	66.6	14.5	1276	4 US-09-909-547-3	Sequence 3, Appli
21	64.2	14.0	1161	4 US-09-552-204A-1	Sequence 1, Appli
22	56.6	12.3	1052	4 US-09-312C-358	Sequence 358, App
23	56.6	12.3	1107	3 US-09-188-930-217	Sequence 217, App
24	56.6	12.3	1107	4 US-09-312-283C-217	Sequence 217, App
25	49.6	10.8	729	4 US-09-336-536-9	Sequence 9, Appli
26	49.6	10.8	1263	4 US-09-336-536-8	Sequence 8, Appli
27	48	10.5	1001	3 US-09-188-930-218	Sequence 218, App

RESULT 1	ALIGNMENTS					
US-09-415-551-2	; Sequence 2, Application US/09415551					
	; Patent No. 6369225					
	; GENERAL INFORMATION:					
	; APPLICANT: Cheah, Kathryn					
	; TITLE OF INVENTION: USES OF TRANSGENIC ANIMALS CONTAINING A TYPE X COLLAGEN					
	; FILE REFERENCE: 57114-A					
	; CURRENT APPLICATION NUMBER: US/09/415, 551					
	; CURRENT FILING DATE: 1999-10-08					
	; NUMBER OF SEQ ID NOS: 5					
	; SOFTWARE: PatentIn Ver. 2.0					
	; SEQ ID NO 2					
	; LENGTH: 459					
	; TYPE: DNA					
	; ORGANISM: mouse					
US-09-415-551-2						
	Query Match	100.0%	Score 459;	Best Local Similarity 100.0%;	Pred. No. 1..1e-15;	DB 4; Length 459;
	Matches 459	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	GTCAATGCCCTGATGGCTCATAAAGCAAGGCCAGGCTTCGGATGCCGCTT	60			
Db	1	GTCAATGCCCTGATGGCTCATAAAGCAAGGCCAGGCTTCGGATGCCGCTT	60			
Qy	61	GTCAATGCCCTGATGGCTCATAAAGCAAGGCCAGGCTTCGGATGCCGCTT	120			
Db	61	GTCAATGCCCTGATGGCTCATAAAGCAAGGCCAGGCTTCGGATGCCGCTT	120			
Qy	121	AAAGCTTACCCGAGTAGGTGGCCCATCCCATGGATCTACATAGGAG 180				
Db	121	AAAGCTTACCCGAGTAGGTGGCCCATCCCATGGATCTACATAGGAG 180				
Qy	181	CAGCATAGGCTACGACGATCTGCTGATCTGCTGATCTGCTGATCTGCTG 240				
Db	181	CAGCATAGGCTACGACGATCTGCTGATCTGCTGATCTGCTGATCTGCTG 240				
Qy	301	CGTATGATGAGTACAGGAAAGGCTACCTGGATCAGGCTTCAGGAAGTCAATCGGAGC 360				
Db	301	CGTATGATGAGTACAGGAAAGGCTACCTGGATCAGGCTTCAGGAAGTCAATCGGAGC 360				
Qy	361	TCAAGAAAATGACCAAGGTATGGCTCCAAATGAGAATCAACGGCCCTCTACT 420				

RESULT 2  
 Sequence 1, Application US/09415551  
 GENERAL INFORMATION:  
 APPLICANT: Cheah, Kathryn  
 APPLICANT: Cheung, Kenneth  
 TITLE OF INVENTION: USES OF TRANSGENIC ANIMALS CONTAINING A TYPE X COLLAGEN  
 TITLE OF INVENTION: MUTANT  
 FILE REFERENCE: 57114-A  
 CURRENT APPLICATION NUMBER: US/09/415,551  
 CURRENT FILING DATE: 1999-10-08  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 486  
 TYPE: DNA  
 ORGANISM: mouse  
 SEQ ID NO 15-551-1  
 Query Match 95.0% Score 436; DB 4; Length 486;  
 Best Local Similarity 97.28% Pred. No. 2.2e-147;  
 Matches 459; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 1 GTCATGCCCTGATGGCTCATAAAGCAGGCCAGGGTACAGGTATGCCGTTACTGTATTCTCTCT 60  
 1 GTCATGCCCTGATGGCTCATAAAGCAGGCCAGGGTACAGGTATGCCGTTACTGTATTCTCTCT 60  
 61 GTCACTGGTAAACCAGGGTAACAGGTATGCCGTTACTGTATTCTCTCT 120  
 61 GTCACTGGTAAACCAGGGTAACAGGTATGCCGTTACTGTATTCTCTCT 120  
 121 AAAGCTTACCCAGGAGTAGGTGCCCCATCCATTGATGAGATTGTACAATAGGCAG 180  
 121 AAAGCTTACCCAGGAGTAGGTGCCCCATCCATTGATGAGATTGTACAATAGGCAG 180  
 121 AAAGCTTACCCAGGAGTAGGTGCCCCATCCATTGATGAGATTGTACAATAGGCAG 180  
 181 CAGGATTAGCCAAAGATCTGGPATCTTACCTGTAAGTCCAGGATATACATTTC 240  
 181 CAGGATTAGCCAAAGATCTGGPATCTTACCTGTAAGTCCAGGATATACATTTC 240  
 241 TCCCTAACCTGGATGTGAAAGGGACTCACGGTTGGTAGCCGTATAAACAGGCAG 300  
 241 TCCCTAACCTGGATGTGAAAGGGACTCACGGTTGGTAGCCGTATAAACAGGCAG 300  
 301 CCTAACGATGTAACGGTACATGAGTAACGAAAGGTACGGTACGGGAT 360  
 348 GCAATCATGGAGCTCACAGAAATGACCAAGGTATGGCTCAATTGCCAAATGCA 407  
 361 GCAATCATGGAGCTCACAGAAATGACCAAGGTATGGCTCAATTGCCAAATGCA 420  
 408 AACGGGCTCTACTCTCTGAGTAGTCCACTGTCAGGTTCCAGGATTCCTAG 459  
 421 AACGGGCTCTACTCTCTGAGTAGTCCACTGTCAGGTTCCAGGATTCCTAG 472

RESULT 3  
 US-09-620-312D-160  
 Sequence 167, Application US/09620312D  
 Patent No. 6569662  
 GENERAL INFORMATION:  
 APPLICANT: Ren, Feiyan  
 APPLICANT: Chen, Rui-hong  
 APPLICANT: Zhao, Qing A.  
 APPLICANT: Wehrman, Tom  
 APPLICANT: Xue, Aidong J.  
 APPLICANT: Yang, Yonghong  
 APPLICANT: Wang, Jian-Rui  
 APPLICANT: Zhou, Ping  
 APPLICANT: Ma, Yunqing  
 APPLICANT: Wang, Dunrui  
 APPLICANT: Wang, Zhivei  
 APPLICANT: John Tillinghast  
 APPLICANT: Drmanac, Radoje T.  
 TITLE OF INVENTION: No. 6566620 Nucleic Acids and  
 TITLE OF INVENTION: Polypeptides  
 FILE REFERENCE: 784CIPB  
 CURRENT APPLICATION NUMBER: US/09/620,312D  
 CURRENT FILING DATE: 2000-07-19  
 PRIORITY NUMBER: 09/552,317  
 PRIORITY FILING DATE: 2000-04-25  
 PRIORITY NUMBER: 09/488,725  
 PRIORITY FILING DATE: 2000-01-21  
 NUMBER OF SEQ ID NOS: 1105  
 SOFTWARE: pt\_FL\_genes Version 1.0  
 SEQ ID NO 160  
 LENGTH: 2487  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (235) .. (2469)  
 US-09-620-312D-160  
 Query Match 29.0% Score 133; DB 4; Length 2487;  
 Best Local Similarity 62.1%; Prod. No. 1.5e-37;  
 Matches 234; Conservative 0; Mismatches 130; Indels 13; Gaps 1;  
 95 TGTCTGGTTTACTGTATTCTCTCTAAAGCTTACCAAGCAGTAGGTGCCCTCATCCAT 154  
 2078 TGCTCTGATTTACCGCCGAGCTACCGCAGCTTCCACCGGCGCCAGTGAAGT 2137  
 155 TGTATGAGATCTGTGATCATAGGAGCAGCATTACGACCAAGATCTGTATCTTACCT 214  
 2138 TTAACAAACTGCTGTATAAGAAC------GGCACAGGATCTTCACCT 2197  
 215 GAAAGATTCAGGGATATACATTCTCTTACCACTGATGAAAGGACTACAGTT 274  
 2198 GTAGGGCTCTGGTCTACTTGTGATACCTTGTGATACCCGTTACTGCAAGGGGGCAAGGTG 2257  
 2258 GGTTGGCTCTTACCAAGAACAAACGAGCCGTGATGTAACGAGTACAAAAGG 2317  
 322 GCTACCTGGATCAGGCTCAGGAGTCACTATGGAGCTCACGAAATGACCAAGTAT 381  
 2318 GCTTCCTGGACGGCACTGGAGTCACTGGCTGTCAGGCTGGAGACGGGTGT 2377  
 382 GGCTCCAAATTGCCAAATGCAAAAGGCCCTCTACTCTCTGAGTAGTCCACTCTG 441  
 2378 TCTTCAGATGCCCTGAGACGGTCAAGGACTGTATGCCAAATGTCACCTCT 2437  
 442 CCTTCCTCAGGATTCTCTA 458  
 2438 CCTTTACGATATTAA 2454

RESULT 4  
 US-09-552-204A-10  
 Sequence 10, Application US/0952204A  
 Patent No. 6569662  
 GENERAL INFORMATION:  
 APPLICANT: Drmanac, Radoje T.  
 APPLICANT: John Tillinghast  
 APPLICANT: Drmanac, Radoje T.  
 TITLE OF INVENTION: No. 6566620 Nucleic Acids and  
 TITLE OF INVENTION: Polypeptides  
 FILE REFERENCE: 784CIPB  
 CURRENT APPLICATION NUMBER: US/09/620,312D  
 CURRENT FILING DATE: 2000-07-19  
 PRIORITY NUMBER: 09/552,317  
 PRIORITY FILING DATE: 2000-04-25  
 PRIORITY NUMBER: 09/488,725  
 PRIORITY FILING DATE: 2000-01-21  
 NUMBER OF SEQ ID NOS: 1105  
 SOFTWARE: pt\_FL\_genes Version 1.0  
 SEQ ID NO 160  
 LENGTH: 2487  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (235) .. (2469)  
 US-09-620-312D-160  
 Query Match 29.0% Score 133; DB 4; Length 2487;  
 Best Local Similarity 62.1%; Prod. No. 1.5e-37;  
 Matches 234; Conservative 0; Mismatches 130; Indels 13; Gaps 1;  
 95 TGTCTGGTTTACTGTATTCTCTCTAAAGCTTACCAAGCAGTAGGTGCCCTCATCCAT 154  
 2078 TGCTCTGATTTACCGCCGAGCTACCGCAGCTTCCACCGGCGCCAGTGAAGT 2137  
 155 TGTATGAGATCTGTGATCATAGGAGCAGCATTACGACCAAGATCTGTATCTTACCT 214  
 2138 TTAACAAACTGCTGTATAAGAAC------GGCACAGGATCTTCACCT 2197  
 215 GAAAGATTCAGGGATATACATTCTCTTACCACTGATGAAAGGACTACAGTT 274  
 2198 GTAGGGCTCTGGTCTACTTGTGATACCTTGTGATACCCGTTACTGCAAGGGGGCAAGGTG 2257  
 2258 GGTTGGCTCTTACCAAGAACAAACGAGCCGTGATGTAACGAGTACAAAAGG 2317  
 322 GCTACCTGGATCAGGCTCAGGAGTCACTATGGAGCTCACGAAATGACCAAGTAT 381  
 2318 GCTTCCTGGACGGCACTGGAGTCACTGGCTGTCAGGCTGGAGACGGGTGT 2377  
 382 GGCTCCAAATTGCCAAATGCAAAAGGCCCTCTACTCTCTGAGTAGTCCACTCTG 441  
 2378 TCTTCAGATGCCCTGAGACGGTCAAGGACTGTATGCCAAATGTCACCTCT 2437  
 442 CCTTCCTCAGGATTCTCTA 458  
 2438 CCTTTACGATATTAA 2454

; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP2  
 ; FILE REFERENCE: 99-08  
 ; CURRENT APPLICATION NUMBER: US/09/552,204A  
 ; PRIORITY APPLICATION NUMBER: 2000-04-19  
 ; PRIORITY FILING DATE: 2000-04-19  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 10  
 ; LENGTH: 855  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Degenerate nucleotide sequence encoding the  
 ; NAME/KEY: variation  
 ; LOCATION: (1)...(855)  
 ; OTHER INFORMATION: Each N is independently any nucleotide.  
 US-09-552-204A-10

Query Match 19.8%; Score 90.8; DB 4; Length 855;  
 Best Local Similarity 35.3%; Pred. No. 1.5e-22;  
 Matches 129; Conservative 70; Mismatches 156; Indels 10; Gaps 1;  
 US-08-463-911-6

Qy 77 GGGTAAACAGGTATGCCGTGTCCTTCTACTGTCAATTCTCTAAAGCTTACCCAGCAG 136  
 Db 428 GYGGWWSNGNCAYACNAARWSNCNTYWSNGINGCNCNAARNNTAYCCNMRNG 487  
 Qy 137 TAGGTGCCCATCCATTGATGAGATCTGTCAATAGGCAGCAGATTAGACCCAA 196  
 Db 488 ARMNYNTNCNNCAARTAARTYGYATAARTYNTATGAAARGGGNGCAYTAAYGENW 547  
 Qy 197 GATGTGGTAACCTTAACTGTAAGATCCCTACACAGCTGTATG 256  
 Db 548 SNWNGNGNARRTYGTNTGYGGNGTNCNGNNAHTTAYTAYTAYGATATHANCY 607  
 Qy 257 TGAAGGGACTCACTGTTGGTAGGCCCTATATAAGAACGGCACAGTATGAGTAC- 314  
 Db 608 TNGNNAATGCAATYTINGNATHGNYNTGNCAYAAGGNCATAYGNATHGNANT 667  
 Qy- 315 -----AGCAAAGGCTACTGGATCAGGCTTCAGGGAGTGCATGAGSTCAG 366  
 Db 668 TYGAGCNAAYACNGNAAYCAYGTGNCNWNGNWSNACRNATHYNGCNYNAARC 727  
 Qy 367 AAATGACGAGGATGGCTTACATGGCCATTGAGAATCAGGCCTCTACTCCCTGTG 426  
 Db 728 ARGNGAYGARGTNTGGYNCARATHTYTAYWNSNGCARAAYGGNTNTTYTAYGAYC 787  
 Qy 427 AGTAC 431  
 Db 788 CNTAY 792

RESULT 5  
 US-08-463-911-6  
 ; Sequence 6, Application US/08463911  
 ; Patent No. 5,963,330  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Scherer, Philipp E.  
 ; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: Two Militia Drive  
 ; CITY: Lexington  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02173

; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/463,911  
 FILING DATE:  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Granahan, Patricia  
 REGISTRATION NUMBER: 32,227  
 REFERENCE/DOCKET NUMBER: WHI95-05  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 861-6240  
 TELEFAX: (617) 861-9540  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1313 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)

Query Match 15.0%; Score 69; DB 2; Length 1313;  
 Best Local Similarity 55.6%; Pred. No. 1.e-14;  
 Matches 183; Conservative 0; Mismatches 130; Indels 16; Gaps 2;  
 Qy 145 CCCATCCATTGATGAGATCTGTCAATAGGCAGCAGATTAGACCCAAAGATCTGCTG 204  
 Db 457 CCCATTTGCTTACCAAGATCTCTACATGACCAAAACCATATGAGCTCCACCTG 516  
 Qy 205 ATCTTACCTGTAAGATCCAGGATATACTATTCTACACGTCATGTGAAAGGG 264  
 Db 517 AAAATCACAATGCAATTCCTGGCTGTACTCTTGCACATACAGCTTATATG 576  
 Qy 265 ACTCACGTTGGTAGGCCTGATAAGAACGGCA-----CACGPATGATGAG 311  
 Db 577 AAGGATGCAAGGTAGCCTCTCAAGAGGAAGGGCTATGCTCTACCTPATGATCAG 636  
 Qy 312 TACAGAAAGGTACTGGATCAGGCTTCAGGGATCAGGATGAAATCATGGACTCAGAAAT 371  
 Db 637 TACCGAAAATAATGTGACCGGGCTCTGGCTCTGCTCATGCTGAGGTGGGC 696  
 Qy 372 GACCAAGGTGGCTCAATTG---CCCATGGAGAAATGAAACGGCCTACTCCTCTG 428  
 Db 697 GACAAAGTGGTCAAGGTATGGAAAGGAGGAAATGACTATGCTATGTGATAAT 756  
 Qy 429 TAGTCACACTGCTCCTCTCAGGATTCT 457  
 Db 757 GACAAATGACTCCACCTCACAGGCTTCT 785

RESULT 6  
 US-09-140-804-9  
 ; Sequence 9, Application US/09140804  
 ; Patent No. 6,197,930  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lodish, Harvey F.  
 ; APPLICANT: Shppard, Paul O.  
 ; APPLICANT: Rumes, Jacqueline M.  
 ; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
 ; FILE REFERENCE: 97-49  
 ; CURRENT APPLICATION NUMBER: US/09/140,804  
 ; CURRENT FILING DATE: 1998-08-26  
 ; EARLIER APPLICATION NUMBER: 60/056,983  
 ; EARLIER FILING DATE: 1997-08-26  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 9  
 ; LENGTH: 4517  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

US-09-140-804-9

Query Match 15.0%; Score 69; DB 3; Length 4517;  
Best Local Similarity 55.6%; Pred. No. 2.8e-14;  
Matches 183; Conservative 0; Mismatches 130; Indels 16; Gaps 2;

Qy 145 CCCATCCATTGATGAGATTCTGACATAGGCAGCAGATTAGCACCAGATCTGGT 204  
Db 411 CCCATTGCTTACAGATCTCTACATAGCAAAACCATATGAGGTCATGT 470

Qy 205 ATCTTACCTGTAAGATCCAGGCTATACATTCTCTACACCTGATGAGGG 264  
Db 471 AAATTCCATGACATTCGGCTTACACTTCCTACACATCACCTATATG 530

Qy 265 ACTCAGTTGGTAGCCTGATAGAACGCA 311  
Db 531 AAGGATGTAAAGCTCAGCTCTCAAGAGCAAGGCATCTCCTACCTATGTCAG 590

Qy 312 TAGGAAAGGCTACCTGATAGGGCTTACGGGAGTCGAATATGGAGCTCAGAAAT 371  
Db 591 TAGGAAAGGAAATATGCGACAGGCTCCGGCGCTCTGCTGAGTCGGCG 650

Qy 372 GACCAGGTAGCTCCATTGAGATCCGGCTCTGCTCTGCTGAGTCGGCG 428  
Db 651 GACCAGGTCTGGCTCCAGGTATGGGAAGGGAGCTATGCTGATAAT 710

Qy 429 TAGCTTACCTGTAAGATCCAGGCTATACATTCTCTACATCACCTATATG 457  
Db 711 GACATATGACTCCACCTTCACAGCTTCT 739

RESULT 8  
US-09-776-976-5  
; Sequence 5, Application US/09776976  
; Patent No. 6566332  
; GENERAL INFORMATION:  
; APPLICANT: Fruebis, Joachim  
; APPLICANT: Erickson, Mary Ruth  
; APPLICANT: Yen, Frances  
; APPLICANT: Bihain, Bernard  
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass  
; FILE REFERENCE: 76 USA REG  
; CURRENT APPLICATION NUMBER: US/09/776,976  
; CURRENT FILING DATE: 2001-02-05  
; PRIORITY NUMBER: US 09/7758,055  
; PRIORITY FILING DATE: 2001-01-10  
; PRIORITY APPLICATION NUMBER: US 60/176,228  
; PRIORITY FILING DATE: 2000-01-14  
; PRIORITY APPLICATION NUMBER: US 60/198,087  
; PRIORITY FILING DATE: 2000-04-13  
; PRIORITY APPLICATION NUMBER: US 60/299,881  
; PRIORITY FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent-2m  
; SEQ ID NO 5  
; LENGTH: 4517  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-776-976-5

Query Match 15.0%; Score 69; DB 4; Length 4517;  
Best Local Similarity 55.6%; Pred. No. 2.8e-14;  
Matches 183; Conservative 0; Mismatches 130; Indels 16; Gaps 2;

Qy 145 CCCATCCATTGATGAGATTCTGACATAGGCAGCAGATTAGCACCAGATCTGGT 204  
Db 411 CCCATTGCTTACAGATCTCTACATCACCAAAACCATATGAGGTCCTACTGGT 204

Qy 205 ATCTTACCTGTAAGATCCAGGCTATACATTCTCTACATCACCTATATG 264  
Db 471 AAATTCCACTGCAACATCTGGCTGACTACTTGTGCTACATGCTTACATCACCTATATG 530

Qy 265 ACTCAGTTGGTAGCCTGATAGAACGCA 311  
Db 531 AAGGATGTAAAGCTCAGCTCTCAAGAGGAAGGGAGCTATGCTGATAAT 590

RESULT 9  
US-09-919-547-5  
; Sequence 5, Application US/09909547  
; Patent No. 657852  
; GENERAL INFORMATION:



RESULT 11  
 US-09-776-976-7  
 Sequence 7, Application US/09776976  
 Patent No. 6566332  
 GENERAL INFORMATION:  
 APPLICANT: Truebis, Joachim  
 APPLICANT: Erickson, Mary Ruth  
 APPLICANT: Yen, Frances  
 APPLICANT: Bihain, Bernard  
 TITLE OF INVENTION: OBC3 Globular Head and Uses Thereof for Decreasing Body Mass  
 CURRENT APPLICATION NUMBER: US/09/776,976  
 CURRENT FILING DATE: 2001-02-05  
 PRIOR APPLICATION NUMBER: US 09/158,055  
 PRIOR FILING DATE: 2001-01-10  
 PRIOR APPLICATION NUMBER: US 60/176,228  
 PRIOR FILING DATE: 2000-01-14  
 PRIOR APPLICATION NUMBER: US 60/198,087  
 PRIOR FILING DATE: 2000-04-13  
 PRIOR APPLICATION NUMBER: US 60/299,881  
 PRIOR FILING DATE: 2000-09-01  
 NUMBER OF SEQ ID NOS: 7  
 SEQ ID NO: 7  
 LENGTH: 20966  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE: misc\_feature  
 LOCATION: 1..4811  
 OTHER INFORMATION: 5' regulatory region  
 NAME/KEY: exon  
 LOCATION: 4812..4851  
 OTHER INFORMATION: exon 1  
 NAME/KEY: exon  
 LOCATION: 15144..15365  
 OTHER INFORMATION: exon 2  
 NAME/KEY: exon  
 LOCATION: 16277..20559  
 OTHER INFORMATION: exon 3  
 NAME/KEY: misc\_feature  
 LOCATION: 20560..20966  
 OTHER INFORMATION: 3', regulatory region  
 NAME/KEY: allele  
 LOCATION: 3787  
 OTHER INFORMATION: 9-27-261 : polymorphic base G or C  
 NAME/KEY: allele  
 LOCATION: 1111  
 OTHER INFORMATION: 99-14387-129 : polymorphic base A or C  
 NAME/KEY: allele  
 LOCATION: 15120  
 OTHER INFORMATION: 9-12-48 : polymorphic base C or T  
 NAME/KEY: allele  
 LOCATION: 15196  
 OTHER INFORMATION: 9-12-124 : polymorphic base G or T  
 NAME/KEY: allele  
 LOCATION: 15427  
 OTHER INFORMATION: 9-12-355 : polymorphic base G or T  
 NAME/KEY: allele  
 LOCATION: 15500  
 OTHER INFORMATION: 9-12-428 : polymorphic base A or G  
 NAME/KEY: allele  
 LOCATION: 15863  
 OTHER INFORMATION: 99-14405-105 : polymorphic base A or G  
 NAME/KEY: allele  
 LOCATION: 17170  
 OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A  
 NAME/KEY: primer\_bind  
 LOCATION: 3528..3545  
 OTHER INFORMATION: 9-27..pu  
 NAME/KEY: primer\_bind  
 LOCATION: 3928..3946  
 OTHER INFORMATION: 9-12-124..mis complement  
 OTHER INFORMATION: 9-27..rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 10990..11008  
 OTHER INFORMATION: 99-14387..pu  
 NAME/KEY: primer\_bind  
 LOCATION: 11423..11442  
 OTHER INFORMATION: 99-14387..rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15073..15092  
 OTHER INFORMATION: 9-12..pu  
 NAME/KEY: primer\_bind  
 LOCATION: 15503..15520  
 OTHER INFORMATION: 9-12..rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15759..15776  
 OTHER INFORMATION: 9-16..pu  
 NAME/KEY: primer\_bind  
 LOCATION: 16191..16211  
 OTHER INFORMATION: 99-14405..rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 16982..17001  
 OTHER INFORMATION: 9-16..pu  
 NAME/KEY: primer\_bind  
 LOCATION: 17384..17402  
 OTHER INFORMATION: 9-16..rp complement  
 NAME/KEY: misc\_binding  
 LOCATION: 3775..3799  
 OTHER INFORMATION: 9-27-261..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 11106..11130  
 OTHER INFORMATION: 99-14387-129..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 15108..15132  
 OTHER INFORMATION: 9-12-48..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 15184..15208  
 OTHER INFORMATION: 9-12-124..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 15415..15439  
 OTHER INFORMATION: 9-12-355..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 1548..15512  
 OTHER INFORMATION: 9-12-428..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 15551..15875  
 OTHER INFORMATION: 99-14405-105..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 17158..17182  
 OTHER INFORMATION: 9-16-189..probe  
 NAME/KEY: primer\_bind  
 LOCATION: 3768..3786  
 OTHER INFORMATION: 9-27-261..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 3788..3806  
 OTHER INFORMATION: 9-27-261..mis complement  
 NAME/KEY: primer\_bind  
 LOCATION: 11099..11117  
 OTHER INFORMATION: 99-14387-129..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 11119..11137  
 OTHER INFORMATION: 99-14387-129..mis complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15101..15119  
 OTHER INFORMATION: 9-12-48..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 15121..15139  
 OTHER INFORMATION: 9-12-48..mis complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15177..15195  
 OTHER INFORMATION: 9-12-124..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 15197..15215  
 OTHER INFORMATION: 9-12-124..mis complement

NAME/KEY: primer\_bind  
 LOCATION: 15408\_15426  
 OTHER INFORMATION: 9-12-355.mis

NAME/KEY: primer\_bind  
 LOCATION: 15428\_15446  
 OTHER INFORMATION: 9-12-355.mis complement

NAME/KEY: primer\_bind  
 LOCATION: 15481\_15499  
 OTHER INFORMATION: 9-12-428.mis

NAME/KEY: primer\_bind  
 LOCATION: 15501\_15519  
 OTHER INFORMATION: 9-12-428.mis complement

NAME/KEY: primer\_bind  
 LOCATION: 15844\_15862  
 OTHER INFORMATION: 9-14405-105.mis

NAME/KEY: primer\_bind  
 LOCATION: 15864\_15882  
 OTHER INFORMATION: 9-14405-105.mis complement

NAME/KEY: primer\_bind  
 LOCATION: 17151\_17169  
 OTHER INFORMATION: 9-16-189.mis

NAME/KEY: primer\_bind  
 LOCATION: 17171\_17189  
 OTHER INFORMATION: 9-16-189.mis complement

US-09-776-976-7

Query Match 15.0% ; Score 69; DB 4; Length 20966;  
 Best Local Similarity 55.6%; Pred. No. 6.4e-14;  
 Matches 183; Conservative 0; Mismatches 130; Indels 16; Gaps 2;

Qy 145 CCCATCCATTGATGAGATCTGTACATAATAGGGAGGCAATTAGCAGCCAAAGATCTGT 204  
 Db 16447 CCCATTGGTTACAGATCTTACATGAGGATGCTGATGTTGCTGAGCTGTT 16506  
 Qy 205 ATCTTACTGTAAAGATCCAGGCTATACTATTCTCTCTACATGAGGATGCTGATGTT 264  
 Db 16507 AAATTCACAGCACATTCTGGCTGTACTACTTGCCTACACATGAGCTATATG 16566  
 Qy 265 ATCTACGTTGGTAGGGCTGTAGAACGG 311  
 Db 16567 AAGATGTGAAAGGTCAGGCTCTCAAGAGGAAGGGCTATGCTCTAACATGATGAG 16626  
 Qy 312 TAAGCAAGGTACCTGTACGGGTCTAGGGAGTGGCAATCATGGAGCTCACAGAAAT 371  
 Db 16627 TRACAGGAATAATATGSGCAGGCTCGGTCTGCTGCTGATCTGGGTGGC 16686  
 Qy 372 GACCGGTATGGCTCCAATTG---CCCATATGAGAATAAACGGCCCTACTCTCTGAG 428  
 Db 16687 GACAAAGTGGCTCAAGGTATGGGAAAGGGAGGCTATGCTATGTGATAAT 16746  
 Qy 429 TAGTCTCACTCGNCCCTCTCAAGGATTC 457  
 Db 16747 GACAATGACTCACCTAACGGCTTCT 16775

RESULT 12  
 US-09-909-547-7  
 Sequence 7, Application US/09909547  
 Patent No. 6579852  
 GENERAL INFORMATION:  
 APPLICANT: Frubis, Joachim  
 APPLICANT: Erickson, Mary Ruth  
 APPLICANT: Yen, Frances  
 APPLICANT: Bihin, Bernard  
 TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass  
 FILE REFERENCE: 76 US6 CIP  
 CURRENT APPLICATION NUMBER: US/09/909,547  
 PRIOR APPLICATION NUMBER: US/09/909,547  
 PRIOR FILING DATE: 2001-07-19  
 PRIOR APPLICATION NUMBER: US/09/776,976  
 PRIOR FILING DATE: 2001-02-05  
 PRIOR APPLICATION NUMBER: US/09/758,055  
 PRIOR FILING DATE: 2001-01-10  
 PRIOR APPLICATION NUMBER: US/09/299,881  
 OTHER INFORMATION: 9-14405.pu

NAME/KEY: primer\_bind  
 LOCATION: 1..4811  
 OTHER INFORMATION: 5' regulatory region  
 NAME/KEY: exon  
 LOCATION: 812..4851  
 OTHER INFORMATION: exon 1  
 NAME/KEY: exon  
 LOCATION: 15144..15365  
 OTHER INFORMATION: exon 2  
 NAME/KEY: exon  
 LOCATION: 16277..20559  
 OTHER INFORMATION: exon 3  
 NAME/KEY: misc feature  
 LOCATION: 20560..20966  
 OTHER INFORMATION: 3' regulatory region  
 NAME/KEY: allele  
 LOCATION: 3787  
 OTHER INFORMATION: 9-27-261 : polymorphic base G or C  
 NAME/KEY: allele  
 LOCATION: 11118  
 OTHER INFORMATION: 99-14387-129 : polymorphic base A or C  
 NAME/KEY: allele  
 LOCATION: 15120  
 OTHER INFORMATION: 9-12-48 : polymorphic base C or T  
 NAME/KEY: allele  
 LOCATION: 15196  
 OTHER INFORMATION: 9-12-124 : polymorphic base G or T  
 NAME/KEY: allele  
 LOCATION: 15427  
 OTHER INFORMATION: 9-12-355 : polymorphic base G or T  
 NAME/KEY: allele  
 LOCATION: 15500  
 OTHER INFORMATION: 9-12-428 : polymorphic base A or G  
 NAME/KEY: allele  
 LOCATION: 15633  
 OTHER INFORMATION: 99-14405-105 : polymorphic base A or G  
 NAME/KEY: allele  
 LOCATION: 17170  
 OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A  
 NAME/KEY: primer\_bind  
 LOCATION: 3528..3545  
 OTHER INFORMATION: 9-27.pu  
 NAME/KEY: primer\_bind  
 LOCATION: 3328..3346  
 OTHER INFORMATION: 9-27.rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15073..15092  
 OTHER INFORMATION: 9-12.pu  
 NAME/KEY: primer\_bind  
 LOCATION: 15503..15520  
 OTHER INFORMATION: 9-12.rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15759..15776  
 OTHER INFORMATION: 99-14405.pu  
 NAME/KEY: primer\_bind

LOCATION: 16191..16211  
 OTHER INFORMATION: 99-14405..105 .rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 16982..17001  
 OTHER INFORMATION: 9-16..16..pu  
 NAME/KEY: primer\_bind  
 LOCATION: 17384..17402  
 OTHER INFORMATION: 9-16..rp complement  
 NAME/KEY: misc\_binding  
 LOCATION: 3775..3799  
 OTHER INFORMATION: 9-27-261..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 11106..11130  
 OTHER INFORMATION: 99-14387-129..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 15108..15132  
 OTHER INFORMATION: 9-12-48..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 15184..15208  
 OTHER INFORMATION: 9-12-124..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 15415..15439  
 OTHER INFORMATION: 9-12-355..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 15488..15512  
 OTHER INFORMATION: 9-12-428..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 15851..15875  
 OTHER INFORMATION: 99-14405-105..probe  
 NAME/KEY: misc\_binding  
 LOCATION: 17151..17182  
 OTHER INFORMATION: 9-16-189..probe  
 NAME/KEY: primer\_bind  
 LOCATION: 3768..3786  
 OTHER INFORMATION: 9-27-261..mis  
 LOCATION: 3788..3806  
 OTHER INFORMATION: 9-27-261..mis complement  
 NAME/KEY: primer\_bind  
 LOCATION: 11099..11117  
 OTHER INFORMATION: 99-14387-129..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 11119..11137  
 OTHER INFORMATION: 99-14387-129..mis complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15101..15119  
 OTHER INFORMATION: 9-12-48..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 15121..15139  
 OTHER INFORMATION: 9-12-48..mis complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15177..15195  
 OTHER INFORMATION: 9-12-124..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 15197..15215  
 OTHER INFORMATION: 9-12-124..mis complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15408..15426  
 OTHER INFORMATION: 9-12-355..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 15428..15446  
 OTHER INFORMATION: 9-12-355..mis complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15481..15499  
 OTHER INFORMATION: 9-12-428..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 15501..15519  
 OTHER INFORMATION: 9-12-428..mis complement  
 NAME/KEY: primer\_bind  
 LOCATION: 15844..15862  
 OTHER INFORMATION: 99-14405-105..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 15864..15882

OTHER INFORMATION: 99-14405-105..mis complement  
 NAME/KEY: primer\_bind  
 LOCATION: 17151..17159  
 OTHER INFORMATION: 9-16-189..mis  
 NAME/KEY: primer\_bind  
 LOCATION: 17191..17199  
 OTHER INFORMATION: 9-16-189..mis complement  
 US-09-909-547-7

Query Match 15.0% Score 69; DB 4; Length 20966;  
 Best Local Similarity 55.6%; Pred. No. 6.4e-14;  
 Matches 183; Conservative 0; Mismatches 130; Indels 16; Gaps 2;

Qy 145 CCCATCCATTGATGAGATTGATCAATAGCAGAGCATTAGCACCAGAATGGATCTCGGT 204  
 Db 16447 CCATTCGCTTACAGATCTTACATCGAAACACTATGATGGCTCCACCTGT 16506  
 Qy 205 ATCTTACCTGTAAAGATCCCAGGATACTACTTCTCCTACACGTGCAATGAAAGGG 264  
 Db 16507 AAATCCACTGAACATCCCTGGCTGTACTTGTGCTACACATCACAGCTATATG 16566

Qy 265 ACTCACGTTGGTAGGCCTGATAGAACGCA-----CAGCTATGATGAG 311  
 Db 16567 AAGGATGTGAAGCTCAGCCTCTCAAGAGGAAAGGCAAGGGTATGGCTTACCTATGATGAG 16626

Qy 312 TAGGCAAGGTTACCTGGATAGGCTCAGCTGGCAATGGAGCTCAGAAAT 371  
 Db 16627 TACAGGAAATAATGAGGACCTGGCTCTGGCTCTGGAGGTGGGC 16686

Qy 372 GACCAAGGTATGGCTCCAATTG--CCCAATGAGAAATCAAACGGCCTACTCTCTCTGAG 428  
 Db 16687 GACAAAGTCTGGTCCAGGTATGGGAAGGAGGCTAATGGACTCTATGCTGATAAT 16746

Qy 429 TACGTCCACTCGTCCTCTCAGGATCTCCT 457  
 Db 16747 GACATGACTCCACCTAACGSCCTCT 16775

RESULT 13  
 US-09-569-852B-1  
 Sequence 1, Application US/09569852B  
 Patent No. 6582909  
 GENERAL INFORMATION:  
 APPLICANT: Bouquelert, Lydie  
 APPLICANT: Bihain, Bernard  
 APPLICANT: Denison, Blake  
 APPLICANT: Yen-Potin, Frances  
 TITLE OF INVENTION: APMI Biallelic Markers and Uses Thereof  
 FILE REFERENCE: GEN-T1113XC2  
 CURRENT APPLICATION NUMBER: US/09/569,852B  
 CURRENT FILING DATE: 2002-03-12  
 PRIOR APPLICATION NUMBER: PCT/IB99/01858  
 PRIOR FILING DATE: 1999-11-04  
 PRIOR APPLICATION NUMBER: US 09/434,848  
 PRIOR FILING DATE: 1999-11-04  
 PRIOR APPLICATION NUMBER: US 60/119,593  
 PRIOR FILING DATE: 1999-02-10  
 PRIOR APPLICATION NUMBER: US 60/107,113  
 PRIOR FILING DATE: 1998-11-04  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 20966  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(481)  
 OTHER INFORMATION: 5', regulatory region  
 NAME/KEY: primer\_bind  
 LOCATION: (14583)..(14701)  
 OTHER INFORMATION: 17-34-860..mis  
 NAME/KEY: primer\_bind

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OTHER INFORMATION: 17-37-629.mis complement
NAME/KEY: primer bind
LOCATION: (14703)_.(14721)
OTHER INFORMATION: 17-34-860.mis complement
NAME/KEY: primer bind
LOCATION: (14738)_.(14756)
OTHER INFORMATION: 17-34-915.mis
NAME/KEY: primer bind
LOCATION: (14739)_.(14776)
OTHER INFORMATION: 17-34-915.mis complement
NAME/KEY: primer bind
LOCATION: (14751)_.(14756)
OTHER INFORMATION: 17-34-915.mis
NAME/KEY: primer bind
LOCATION: (14758)_.(14814)
OTHER INFORMATION: 17-35-71.mis
NAME/KEY: primer bind
LOCATION: (14816)_.(14834)
OTHER INFORMATION: 17-35-71.mis complement
NAME/KEY: primer bind
LOCATION: (15031)_.(15049)
OTHER INFORMATION: 17-35-306.mis
NAME/KEY: primer bind
LOCATION: (15051)_.(15069)
OTHER INFORMATION: 17-35-306.mis complement
NAME/KEY: primer bind
LOCATION: (15101)_.(15119)
OTHER INFORMATION: 9-12-48.mis
NAME/KEY: primer bind
LOCATION: (15121)_.(15139)
OTHER INFORMATION: 9-12-48.mis complement
NAME/KEY: primer bind
LOCATION: (15177)_.(15195)
OTHER INFORMATION: 9-12-124.mis
NAME/KEY: primer bind
LOCATION: (15197)_.(15215)
OTHER INFORMATION: 9-12-124.mis complement
NAME/KEY: primer bind
LOCATION: (15408)_.(15426)
OTHER INFORMATION: 9-12-355.mis
NAME/KEY: primer bind
LOCATION: (15428)_.(15446)
OTHER INFORMATION: 9-12-355.mis complement
NAME/KEY: primer bind
LOCATION: (15481)_.(15499)
OTHER INFORMATION: 9-12-428.mis
NAME/KEY: primer bind
LOCATION: (15501)_.(15519)
OTHER INFORMATION: 9-12-428.mis complement
NAME/KEY: primer bind
LOCATION: (15561)_.(15679)
OTHER INFORMATION: 17-36-47.mis
NAME/KEY: primer bind
LOCATION: (15681)_.(15699)
OTHER INFORMATION: 17-36-47.mis complement
NAME/KEY: primer bind
LOCATION: (15791)_.(15809)
OTHER INFORMATION: 17-36-120.mis complement
NAME/KEY: primer bind
LOCATION: (15844)_.(15862)
OTHER INFORMATION: 99-14405-105.mis
NAME/KEY: primer bind
LOCATION: (17171)_.(17189)
OTHER INFORMATION: 9-16-189.mis complement
NAME/KEY: primer bind
LOCATION: (17810)_.(17828)
OTHER INFORMATION: 17-37-629.mis
NAME/KEY: primer bind
LOCATION: (17830)_.(17848)

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NAME/KEY: primer\_bind  
 LOCATION: (11189). .(11207)  
 OTHER INFORMATION: 99-14387-199.mis complement

NAME/KEY: primer\_bind  
 LOCATION: (13154). .(13972)  
 OTHER INFORMATION: 17-33-TGAGACT.mis

NAME/KEY: primer\_bind  
 LOCATION: (13974). .(13992)  
 OTHER INFORMATION: 17-33-TGAGACT.mis complement

NAME/KEY: exon  
 LOCATION: (4812). .(4851)  
 OTHER INFORMATION:

NAME/KEY: exon  
 LOCATION: (16277). .(20559)  
 OTHER INFORMATION:

NAME/KEY: misc feature  
 LOCATION: (15144). .(15365)  
 OTHER INFORMATION: 3' regulatory region

Query Match 15.0%; Score 69; DB 4; Length 20966;  
 Best Local Similarity 55.6%; Pred. No. 6.4e-14;  
 Matches 183; Conservative 0; Mismatches 130; Indels 16; Gaps 2;

Qy 145 CCCATCCCATTTGATGATTCTTACATAGGAGCCACCATACGACAAAGATCTGT 204  
 Db 16447 CCCATTGGCTTTACAAAGATCTTACATACGAAACCACTATGATG 16506

Qy 205 ATCTTTACCTGTAGATCCAGGATATACATTTCTTACACAGTGTGAAGG 264  
 Db 16507 AAATTCACATGCAATCTGGCTGAACTACTTGTACACATGACGCTATG 16566

Qy 265 ACTCACGTTGGPAGGCCGTATAAGAACGCA-----CAGCTATGATAG 311  
 Db 16567 AAGATGTAAGGCAAGGCCCTTAAGAACGAGGTATGTCCTTACCTATGAG 16626

Qy 312 TACGCCAAGGCTACCTGATCAGGCTTACGGGTGAAATCATGGAGCTCACAGAAAT 371  
 Db 16627 TACCGAAAATAATGTGACCCGGCTCGGGCTCTGGCATCTGGCTGGGC 16686

Qy 372 GACCGAGTATGGTCCATTG--GCCATGCGAATCAAACGGGCTACTCTCTGAG 428  
 Db 16687 GACCAAGTCTGGCTCAGGGTATGGGAGGAATGAACTCTATGTGATAT 16746

Qy 429 TACGTCACACTGTCCTTCAGGATTCT 457  
 Db 16747 GACAATGACTCACCTTACAGGCTTCT 16775

RESULT 15  
 US-09-686-838B-10  
 ; Sequence 10, Application US/09686838B  
 ; Patent No. 6482612

; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; INVENTOR: Humes, Jacqueline M.  
 ; TITLE OF INVENTION: Adipocyte-Specific Protein Homologs  
 ; FILE REFERENCE: 97-49D1  
 ; CURRENT APPLICATION NUMBER: US/09/686,838B  
 ; CURRENT FILING DATE: 2000-10-10  
 ; PRIOR APPLICATION NUMBER: US 09/140,804  
 ; PRIOR FILING DATE: 1998-08-26  
 ; PRIOR APPLICATION NUMBER: US 60/056,983  
 ; PRIORITY FILING DATE: 1997-08-26  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 10  
 ; LENGTH: 729  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Degenerate nucleotide sequence encoding the zsig39

; OTHER INFORMATION: polypeptide of SEQ ID NO:2.

Query Match 14.6%; Score 66.8; DB 4; Length 729;  
 Best Local Similarity 34.4%; Pred. No. 6.3e-14;  
 Matches 123; Conservative 52; Mismatches 16; Gaps 1;

Qy 118 TCTAAAGCTTACCCAGCAGTAGGTGCCCATCCATTGATGAGATTCTGTACAAATAGG 177  
 Db 337 WSNMGRGNTCCNCNNCWNAGCAGNCNNYNCNCCNTYGAAGMGNNTYNTGNAAYGAR 396

Qy 178 CAGCACATTAGACCCAAAGATCTGATCTTCTGTAAGATCCAGGATATACT 237  
 Db 397 CARGGNCAYTAYGAGCNGTNACNGENAAARTTYACNTGYCARGTNCCNGNGNTAYTAY 456

; OTHER INFORMATION: Degenerate nucleotide sequence encoding the zsig39

; OTHER INFORMATION: polypeptide of SEQ ID NO:2.

Qy	238	TTCTCTTACCACTGATGTGAAGGGACTCACCTTGGCTGATTAAGAACGGC	297
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Qy	298	ACACGTATGATGAGTACAGCAAAACGCTAACCTGGATCAGGC-----TTCA	341
Db	517	GARWSNATHGCNWSNNTYTTTCARTTYTGGNGNTGGCNAARCCNGNWSNTNNWSN	576
Qy	342	GGGAGTGCATGAGGCTCACAGAAAATGACCAAGTATGGCTCCAAATGCCCATGCA	401
Db	577	GGNGGNGNATGGTNTMGNYNTGARCCNGARGAYCRGTTNTGGTNCARGTTNGNTNGGN	636
Qy	402	GAAATCAACGGCTCTACTCTGAGTACGTCCACTGTCCTTCAGGATTCTCTAG	459
Db	632	GAYTAYATHGAGNATHAAGCNCNNWNAATHAARACNGNWSNACNTYTTGTTT	694

Search completed: July 20, 2004, 21:16:42  
Job time : 68 secs

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